



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/834,794

Source: OIPE

Date Processed by STIC: 5/8/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/834,294

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/834,794

DATE: 05/08/2001
 TIME: 15:44:28

Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\05082001\I834794.raw

Does Not Comply
 Corrected Diskette Needed

pp1-5

3 <110> APPLICANT: Lawrence, Papsidero
 4 Lyn, Dyster
 5 Jana, Frustaci
 7 <120> TITLE OF INVENTION: Detection and Treatment of Breast Cancer
 9 <130> FILE REFERENCE: 3380/11127-US4
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/834,794
 C--> 12 <141> CURRENT FILING DATE: 2001-04-13
 14 <150> PRIOR APPLICATION NUMBER: 09/146,580
 15 <151> PRIOR FILING DATE: 1998-09-03
 17 <150> PRIOR APPLICATION NUMBER: 60/071,899
 18 <151> PRIOR FILING DATE: 1998-01-20
 20 <150> PRIOR APPLICATION NUMBER: 60/092,155
 21 <151> PRIOR FILING DATE: 1998-07-09
 23 <160> NUMBER OF SEQ ID NOS: 35
 25 <170> SOFTWARE: PatentIn version 3.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 127
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: UNSURE
 34 <222> LOCATION: (70)..(70)
 35 <223> OTHER INFORMATION: Xaa at position 70 is either Arg or Gly
 38 <220> FEATURE:
 39 <221> NAME/KEY: UNSURE
 40 <222> LOCATION: (91)..(91)
 41 <223> OTHER INFORMATION: Xaa at position 70 is either Lys or Asn
 44 <400> SEQUENCE: 1
 46 Met Gln Gln Arg Gly Leu Ala Ile Val Ala Leu Ala Val Cys Ala Ala
 47 1 5 10 15
 49 Leu His Ala Ser Glu Ala Ile Leu Pro Ile Ala Ser Ser Cys Cys Thr
 50 20 25 30
 52 Glu Val Ser His His Ile Ser Arg Arg Leu Leu Glu Arg Val Asn Met
 53 35 40 45
 55 Cys Arg Ile Gln Arg Ala Asp Gly Asp Cys Asp Leu Ala Ala Val Ile
 56 50 55 60
 58 Leu His Val Lys Arg Xaa Arg Ile Cys Val Ser Pro His Asn His Thr
 59 65 70 75 80
 61 Val Lys Gln Trp Met Lys Val Gln Ala Ala Xaa Lys Asn Gly Lys Gly
 62 85 90 95
 64 Asn Val Cys His Arg Lys Lys His His Gly Lys Arg Asn Ser Asn Arg
 65 100 105 110
 67 Ala His Gln Gly Lys His Glu Thr Tyr Gly His Lys Thr Pro Tyr
 68 115 120 125
 70 <210> SEQ ID NO: 2
 71 <211> LENGTH: 104
 72 <212> TYPE: PRT

91 (see below)

OK

RAW SEQUENCE LISTING

DATE: 05/08/2001

PATENT APPLICATION: US/09/834,794

TIME: 15:44:28

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\05082001\I834794.raw

73 <213> ORGANISM: Homo sapiens
 75 <220> FEATURE:
 76 <221> NAME/KEY: UNSURE
 77 <222> LOCATION: (47)..(47)
 78 <223> OTHER INFORMATION: Xaa at position 47 is either Arg or Gly
 81 <220> FEATURE:
 82 <221> NAME/KEY: UNSURE
 83 <222> LOCATION: (68)..(68)
 84 <223> OTHER INFORMATION: Xaa at position (47) is either Lys or Asn *68 (see below)*
 87 <400> SEQUENCE: 2
 89 Leu Pro Ile Ala Ser Ser Cys Cys Thr Glu Val Ser His His Ile Ser
 90 1 5 10 15
 92 Arg Arg Leu Leu Glu Arg Val Asn Met Cys Arg Ile Gln Arg Ala Asp
 93 20 25 30
 95 Gly Asp Cys Asp Leu Ala Ala Val Ile Leu His Val Lys Arg Xaa Arg
 96 35 40 45
 98 Ile Cys Val Ser Pro His Asn His Thr Val Lys Gln Trp Met Lys Val
 99 50 55 60
 101 Gln Ala Ala Xaa Lys Asn Gly Lys Gly Asn Val Cys His Arg Lys Lys
 102 65 70 75 80
 104 His His Gly Lys Arg Asn Ser Asn Arg Ala His Gln Gly Lys His Glu
 105 85 90 95
 107 Thr Tyr Gly His Lys Thr Pro Tyr
 108 100
 110 <210> SEQ ID NO: 3
 111 <211> LENGTH: 18
 112 <212> TYPE: PRT
 113 <213> ORGANISM: Homo sapiens
 115 <400> SEQUENCE: 3
 117 Thr Glu Val Ser His His Ile Ser Arg Arg Leu Leu Glu Arg Val Asn
 118 1 5 10 15
 120 Met Cys
 123 <210> SEQ ID NO: 4
 124 <211> LENGTH: 16
 125 <212> TYPE: PRT
 126 <213> ORGANISM: Homo sapiens
 128 <400> SEQUENCE: 4
 130 Lys Asn Gly Lys Gly Asn Val Cys His Arg Lys Lys His His Gly Lys
 131 1 5 10 15
 133 <210> SEQ ID NO: 5
 134 <211> LENGTH: 19
 135 <212> TYPE: PRT
 136 <213> ORGANISM: Homo sapiens
 138 <400> SEQUENCE: 5
 140 Asn Ser Asn Arg Ala His Gln Gly Lys His Glu Thr Tyr Gly His Lys
 141 1 5 10 15
 143 Thr Pro Tyr
 146 <210> SEQ ID NO: 6
 147 <211> LENGTH: 3117

RAW SEQUENCE LISTING
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DATE: 05/08/2001
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Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\05082001\I834794.raw

148 <212> TYPE: DNA

149 <213> ORGANISM: Homo sapiens

151 <220> FEATURE:

152 <221> NAME/KEY: unsure

153 <222> LOCATION: (1)..(3117)

154 <223> OTHER INFORMATION: n at any position in the sequence may represent a or g or c or (t/

158 <400> SEQUENCE: 6

*see item 3
on Enron summary
sheet*

line exceeds 72-character-limit

W--> 159 aacatcctca cttgtgttgc tgtcagtgcc tgtanggcag gcaggaatgc agcagagagg 60
161 actcgccatc gtggccttgg ctgtctgtgc ggccctacat gcctcagaag ccatacttcc 120
163 cattgcctcc agctgttgca cggaggtttc acatcatatt tccagaaggc tcctggaaag 180
165 agtgaatatg tgtcgcatcc agagagctga tggggattgt gacttggctg ctgtcatcct 240
W--> 167 tcatgtcaag cgcngaagaa tctgtgtcag cccgcacaac catactgtta agcagtggat 300
W--> 169 gaaagtgcga gctgccaana aaaatggtaa aggaaatgtt tgccacagga agaaacacca 360
171 tggcaagagg aacagtaaca gggcacatca ggggaaacac gaaacatacg gccataaaac 420
173 tccttattag agaattctaca gataaatcta cagagacaat cccccaagtg gacttggcca 480
175 tgattggttg taagttttatc atctgaattc tccttattgt agacaacaga aaaaaacaaa 540
177 atattggttt ttaaaaaatg aacaattgtg ccgtatgcaa atgtacccaa taatatactc 600
W--> 179 cactggaaaa tgaatgaaa aaannatact ggctgggtat ggtgggtccc cccttttacc 660
W--> 181 ccannnnctt cgggaggcag aggcaggagg atcacttgag accaggantt ngagacnagc 720
W--> 183 tnggggcaaa anagcaanga cntcatttnt acaaacnaaa aaaaannntt gcccggcntg 780
W--> 185 ctagnacttg cntataatcc cagcnactg ggaggtngag gtgggaggat cacttgagtc 840
W--> 187 tggngaggtt ngaggtnagc gtgagcagcn tgggtgacag aatgnagacc ntgtctctaa 900
W--> 189 aaataataat aataatgata gtgtatatct tcatataata ttttaagnag gagcatatag 960
W--> 191 atataacttn ctcccaactt tttaattata gttttccaaa cttacagaga agttaaaaga 1020
193 atggtacaat gaacatctat atatctttca ccacaatatt aatcattgtt aatattgtgc 1080
W--> 195 cacatttgc tctctctctc tctcttggta ggggttncaa tataaaatat tataactttt 1140
197 aaaaatatatc ttgttttgc aaccattgga aaataagttg caaaaatcat gacacttcac 1200
W--> 199 ccctagtgtt ttttnggtgt tataacttga cataccctaa aataaagaca tttttctaca 1260
201 taatcacctt atcagtttta tacctaaaaa attaataatt tcatctaata tattccatat 1320
203 tcaaattttc ccaactatct agagagcatt ttatgtagtt tttttttcac tccagtaatc 1380
W--> 205 aatcaaggtn gacatacata ttgcaaatat ttgttatatt tctttaatat ctttcaatct 1440
207 aagaaagtgc ctctgtcttt tttttttaat ttttaaaatt attttgttga gggaggggtc 1500
209 tgctgtgtct tccaggtcgg agtgcagtg cacaattttg attttggctc actgaagcct 1560
W--> 211 caacttttag gctcaagcaa tctctccacc tcagcctncc cgagtatctg ggatcaagg 1620
213 gcatacccac cacacctggc taattttgtt tattttttgt agagacaggg tctcactatg 1680
215 ttgcccaggt tgatctcaaa ctctctgggt caagcgatcc tcccacctta gcctocccaa 1740
217 gtactgggat tataggtgtg agccacagtg cctggcctaa ttattttctt gtgatcaaat 1800
219 tcagggtttta tggttttgggt taagaatttc ctacgtgaat tcgtgtactt attttgtcat 1860
221 tttagagttca taaatattag ggtttatttt cttaaataaa tagtttaaac taaatataac 1920
223 ttcaaaaacgt ctagtgttag tagctaccgt tggttggtt gaaattttct gatactgaaa 1980
W--> 225 agaacaaaaa gcctgccttt ctgcccanaa csnnrtgcyt cccccagtna gttcttggng 2040
W--> 227 cagnactagt taggnnccca gagttnggcc ttngkgtgg tgattttang yctgcctaa 2100
W--> 229 acaaggngcn wacatytttt agctcctatt ccaccyttct namamgtttt tgttgtkgtt 2160
W--> 231 tgnttggttt tttkgagaca grrntnnyat ctgtttgccc argctggart tgcagtggca 2220
W--> 233 caatytnngy tncattgcaa cytcngcytc cssgccgttc aaktgatyyt cttgcytcag 2280
W--> 235 cytccccaa taantgatat tacaggngcc cagccaccam accccgntga wttttgtatt 2340
W--> 237 tttartarar amrgggtttt cccgcnttgg cngggctgggt ctcaantcc ttgamctcna 2400
W--> 239 ktgaaccacc cgcctgtgcc ycccaaatg ctggaattac cancggtgan ccaccatgcc 2460
W--> 241 gggcyacac gtttgarttt ganaccattg tnccattcct cttttggcct yttttttntc 2520

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Input Set : A:\Seqlist.txt

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```

W--> 243 catagnngct tcaagataga tangtaagrg cccagtagtn gttcwtarga agcnmatagr 2580
W--> 245 rancrggarc cantttnatc aggtgggcag gtgtccnngg cytcctgct ggytnntccc 2640
W--> 247 aagcgggtgtt gttgccarga nktnttgar gtgataatgg gananaccag naggcmctga 2700
W--> 249 gtyncnntag gttnaaatgc caccaaaact ggcctttggc ctaatatccy ycnttgamta 2760
W--> 251 nttarcattt awttttattwa tttncctgac atttntgcma ncctttgtwt ttntatttcc 2820
W--> 253 nctntatara wgargaaatt tgaggntytt araggtaaaa tganttgcnc nrgtnnacmc 2880
W--> 255 aggaagtggc nraranaanc tttttanatn mgaaaaaatt aataaaatat aatatgagag 2940
W--> 257 taacttaaaa tattaataaa ccacaatttt aaattaatta accgtgataa ccaacattaa 3000
W--> 259 taaaagttaa gataccaaaa cactggtgtn taattttttt aactaacaaan ttgaattatt 3060
W--> 261 ttccatttta aattaattaa ccgtgataac caacattaat aaaagttaag ataccgn 3117
264 <210> SEQ ID NO: 7
265 <211> LENGTH: 381
266 <212> TYPE: DNA
267 <213> ORGANISM: Homo sapiens
269 <220> FEATURE:
270 <221> NAME/KEY: unsure
271 <222> LOCATION: (207)..(207) (208)..(208) "c" is at location 207
272 <223> OTHER INFORMATION: n may represent a or g or c or t/u
275 <220> FEATURE:
276 <221> NAME/KEY: unsure
277 <222> LOCATION: (272)..(272) (273)..(273) "a" is at location 272
278 <223> OTHER INFORMATION: n may represent a or g or c or t/u
281 <400> SEQUENCE: 7
282 atgcagcaga gaggactgc catcgtggcc ttggctgtct gtgcggccct acatgcctca 60
284 gaagccatac ttcccattgc ctccagctgt tgacaggagg ttccacatca tatttccaga 120
286 aggtcctctg aaagagtga tatgtgtgct atccagagag ctgatgggga ttgtgacttg 180
W--> 288 gctgctgtca tcttcatgt caagcgcga agaactctgt tcagcccgca caaccatact 240
W--> 290 gtttaagcagt ggatgaaagt gcaagctgcg aaaaaaatg gtaaggaaa tgtttgccac 300
292 aggaagaaa accatggcaa gaggaacagt aacagggcac atcaggggaa acacgaaaca 360
294 tacggccata aaactcctta t 381
297 <210> SEQ ID NO: 8
298 <211> LENGTH: 104
299 <212> TYPE: DNA
300 <213> ORGANISM: Homo sapiens
302 <400> SEQUENCE: 8
303 acacgaattc acgtaggaaa ttcttaacca aaaacattaa acctgaattt gatcacaaga 60
305 aaataattag gccaggcact gtggctcaca cctataatcc cagt 104
308 <210> SEQ ID NO: 9
309 <211> LENGTH: 25
310 <212> TYPE: DNA
311 <213> ORGANISM: Homo sapiens
313 <400> SEQUENCE: 9
314 gaattcacgt aggaaattct taacc 25
317 <210> SEQ ID NO: 10
318 <211> LENGTH: 22
319 <212> TYPE: DNA
320 <213> ORGANISM: Homo sapiens
322 <400> SEQUENCE: 10
323 actgggatta taggtgtgag cc 22

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/834,794

DATE: 05/08/2001
TIME: 15:44:28

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05082001\I834794.raw

326 <210> SEQ ID NO: 11
327 <211> LENGTH: 311
328 <212> TYPE: DNA
329 <213> ORGANISM: Homo sapiens
331 <220> FEATURE:
332 <221> NAME/KEY: unsure
333 <222> LOCATION: (101)..(101)
334 <223> OTHER INFORMATION: n may be a or g or c or t/u
337 <220> FEATURE:
338 <221> NAME/KEY: unsure
339 <222> LOCATION: (162)..(162)
340 <223> OTHER INFORMATION: n may be a or g or c or t/u
343 <400> SEQUENCE: 11
344 ggagagagcc gtatgtttcg tgtttccct gatgtgccct gttactgttc ctcttgccat 60
346 ggtgtttctt cctgtggcaa acatttcctt taccattttt ntggcagct tgcactttca 120
348 tccactgctt aacagtatgg ttgtgagggc tgacacagat tnttctgccc ttgacatgaa 180
350 ggatgacagc agccaagtca caatcccat cagctctctg gatgcgacac atattcactc 240
352 ttccaggag cctctggaa atatgatgtg aaacctccgt gcaacagctg gaggaatgg 300
354 gaagtatggc t 311
357 <210> SEQ ID NO: 12
358 <211> LENGTH: 20
359 <212> TYPE: DNA
C--> 360 <213> ORGANISM: Artificial
362 <220> FEATURE:
363 <223> OTHER INFORMATION: Sequencing primer T7
365 <400> SEQUENCE: 12
366 taatacgact cactataggg 20
369 <210> SEQ ID NO: 13
370 <211> LENGTH: 18
371 <212> TYPE: DNA
C--> 372 <213> ORGANISM: Artificial
374 <220> FEATURE:
375 <223> OTHER INFORMATION: pCR3.1 Reverse Primer
377 <400> SEQUENCE: 13
378 tagaaggcac agtcgagg 18
381 <210> SEQ ID NO: 14
382 <211> LENGTH: 22
383 <212> TYPE: DNA
C--> 384 <213> ORGANISM: Artificial
386 <220> FEATURE:
387 <223> OTHER INFORMATION: Gene specific primer (24R)
389 <400> SEQUENCE: 14
390 actgggatta taggtgtgag cc 22
393 <210> SEQ ID NO: 15
394 <211> LENGTH: 24
395 <212> TYPE: DNA
C--> 396 <213> ORGANISM: Artificial
398 <220> FEATURE:
399 <223> OTHER INFORMATION: Gene specific primer (24R2)

see item 11 on Eva Summary Sheet

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/834,794

DATE: 05/08/2001
TIME: 15:44:29

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05082001\I834794.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:360 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:372 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:384 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:396 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:408 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:420 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17

VERIFICATION SUMMARY DATE: 05/08/2001
PATENT APPLICATION: US/09/834,794 TIME: 15:44:29

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05082001\I834794.raw

L:432 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:444 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19